

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

10/644,664	
expe	
9-3-04	
	<u>'</u> '

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/644, 664					
ATTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE					
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."					
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.					
3Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.					
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.					
5Variable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.					
6PatentIn 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.					
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)					
	This sequence is intentionally skipped					
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.					
8 Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000					
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.					
10 Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: <u>Unknown</u> , <u>Artificial Sequence</u> , or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence					
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)					
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.					
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.					

AMC/MH - Biotechnology Systems Branch - 08/21/2001



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/644,664

DATE: 09/03/2003 TIME: 16:54:47

Input Set : A:\kuvshinov 1-intron.ST25.txt
Output Set: N:\CRF4\09032003\J64464.raw

C>	5 7 9 9 11 13 14 15	<pre>&lt;110&gt; APPLICANT: UniCrop Ltd &lt;120&gt; TITLE OF INVENTION: A molecular mechanism for gene containment in plants &lt;130&gt; FILE REFERENCE: kuvshinov 1-intron &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/644,664 &lt;141&gt; CURRENT FILING DATE: 2003-08-20 &lt;160&gt; NUMBER OF SEQ ID NOS: 13 &lt;170&gt; SOFTWARE: PatentIn version 3.2 &lt;210&gt; SEQ ID NO: 1 &lt;211&gt; LENGTH: 357 &lt;212&gt; TYPE: DNA</pre> <pre> Does Not Comply Corrected Diskette Need </pre>
	16	<213> ORGANISM: (artificial sequence Bacillus amyloliquefaciens) Summar to the
	18	<220> FEATURE:
		<223> OTHER INFORMATION: Plant adapted synthetic coding sequence of barnase gene
	21	<pre>&lt;400&gt; SEQUENCE: 1 cqcqqatcca tggcacaagt tatcaacacc tttgatggag ttgctgacta ccttcagacc 60</pre>
	24	taccataagc ttccagataa ctacatcacc aagtctgagg ctcaggctct tggatgggtt 120
	24	gcttctaagg gaaaccttgc tgatgtcgct ccaggaaagt ctatcggagg tgatatcttc 180
	28	totaacaggg agggaaagct tocaggaaag totggaagga cotggaggga ggotgatato 240
	30	aactacacct ctggattcag gaactctgat aggatccttt actcttccga ctggcttatc 300
	32	tacaagacca ctgaccacta ccagaccttc accaagatcc ggtgagagct cgagcgc 357
		<210> SEQ ID NO: 2
	36	<211> LENGTH: 299
	37	<212> TYPE: DNA
		<213> ORGANISM: artificial sequence/Bacillus amyloliquefaciens
	40	<220> FEATURE:
		<pre>&lt;223&gt; OTHER INFORMATION: Plant adapted synthetic coding sequence of barstar gene</pre>
	43	<pre>&lt;400&gt; SEQUENCE: 2 cgcggatcct gatcatgaag aaggctgtta tcaacggtga gcaaattagg tctatctctg 60</pre>
	44	atetteacca gaccettaag aaggagettg etetteeaga gtactaegga gagaacettg 120
	40	atgetetatg ggattgeett accggatggg tggagtacce acttgttttg gagtggagge 180
	50	agtttgagca gtctaagcag cttactgaga atggagctga gagtgttctt caggttttcc 240
	52	gggaggctaa ggctgaggga tgcgatatca ccatcattct ttcttgagag ctcgagcgc 299
		<210> SEQ ID NO: 3
		<211> LENGTH: 529
	57	<212> TYPE: DNA
	58	<213> ORGANISM: artificial sequence
		<220> FEATURE:
		<223> OTHER INFORMATION: intron of uidA gene
		<pre>&lt;400&gt; SEQUENCE: 3 actactttac apacetttes statatagas estectttat teactacttt estecetaet 60</pre>
	64	actautitat adatuttee ctatataaa ootoottiga oomoogi ii
	66	diddiling included accordance accordance and an arms
·	68 70	aaaagttagt atggctcaag ttattaatac ttttgatgga gttgctgatt atcttcaaac 180 ttatcataaa cttccagata attatattac taaatctgaa gctcaagctc ttggatgggt 240

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Input Set : A:\kuvshinov 1-intron.ST25.txt
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72 tgcttctaaa ggaaatcttg ctgatgttgc tccaggaaaa tctattggag gagatattt 74 ttcaaataga gaaggaaaac ttccaggaaa atctggaaga acatggagag aagctgatat 76 taattatact tctggattta gaaattcaga tagaatcctt tattcatctg attggcttat 78 ttataaaact acagatcatt atcaaacttt tacaaaaatt agataaatat ttgtatttt 80 tgtatgttgt gatcattaat aaataaataa atacatacct cttctgcag 83 <210> SEQ ID NO: 4 84 <211> LENGTH: 52 85 <212> TYPE: DNA 86 <213> ORGANISM: artificial sequence 88 <220> FEATURE: 89 <223> OTHER INFORMATION: the last (third exon) of uiD gene	300 360 420 480 529
91 <400> SEQUENCE: 4 92 gtggaccggg atgaacttcg gagagaagcc acagcaggga ggaaagcagt ga	52
95 <210> SEQ ID NO: 5	
96 <211> LENGTH: 51	
97 <212> TYPE: DNA	
98 <213> ORGANISM: artificial sequence 100 <220> FEATURE:	
100 <220 FEATURE: 101 <223> OTHER INFORMATION: 5'UTR of barnase gene	
103 <400> SEQUENCE: 5	
104 catcccggtc cacctgcaaa ataagtaata agataaagta aaaaagttag t	51
107 <210> SEQ ID NO: 6	
108 <211> LENGTH: 38	
109 <212> TYPE: DNA	
110 <213> ORGANISM: artificial sequence 112 <220> FEATURE:	
112 <220> FEATORE: 113 <223> OTHER INFORMATION: 3' flanking signal of the intron of uidA	
115 <400> SEQUENCE: 6	
116 actaactttt ttactttatc ttattactta ttttgcag	38
119 <210> SEQ ID NO: 7	
120 <211> LENGTH: 474	
121 <212> TYPE: DNA	
122 <213> ORGANISM: artificial sequence	
124 <220> FEATURE: 125 <223> OTHER INFORMATION: 35 S promoter of CaMV	
127 <400> SEQUENCE: 7	
128 geggaattea attgateaac atggtggage acgaeactet egtetaetee aagaatatea	60
130 aagatacagt ctcagaagac cagagggcta ttgagacttt tcaacaaagg gtaatatcgg	120
132 gaaacctcct cggattccat tgcccagcta tctgtcactt catcgaaagg acagtagaaa	180
134 aggaagatgg cttctacaaa tgccatcatt gcgataaagg aaaggctatc gttcaagaat	240
136 gcctctaccg acagtggtcc caaagatgga cccccaccca cgaggaacat cgtggaaaaa	300
138 gaagacgttc caaccacgtc ttcaaagcaa gtggattgat gtgatatctc cactgacgta	360 420
140 agggatgacg cacaatccca ctatactcta tcactgatag agtctatata agactctatc 142 actgatagag tgaactctat cactgataga gtcgacggat ccatggaatc cgcg	474
145 <210> SEQ ID NO: 8	1/1
146 <211> LENGTH: 10	
147 <212> TYPE: DNA	
148 <213> ORGANISM: artificial sequence	
150 <220> FEATURE:	

## RAW SEQUENCE LISTING PATENT APPLICATION: US/10/644,664 DATE: 09/03/2003 TIME: 16:54:47

Input Set : A:\kuvshinov 1-intron.ST25.txt
Output Set: N:\CRF4\09032003\J644664.raw

```
151 <223> OTHER INFORMATION: sequence upstream the PstI site
    153 <400> SEQUENCE: 8
                                                                                 10
    154 cgcttttctg
    157 <210> SEQ ID NO: 9
    158 <211> LENGTH: 10
    159 <212> TYPE: DNA
    160 <213> ORGANISM: artificial sequence
    162 <220> FEATURE:
    163 <223> OTHER INFORMATION: changed sequence upstream the pstI site
    165 <400> SEQUENCE: 9
                                                                                 10
     166 tgccttcctg
     169 <210> SEQ ID NO: 10
     170 <211> LENGTH: 10
     171 <212> TYPE: DNA
     172 <213> ORGANISM: artificial sequence
     174 <220> FEATURE:
     175 <223> OTHER INFORMATION: polyadenylation signal in transcription unit near the
upstream
               element (NUE)
     176
     178 <400> SEQUENCE: 10
                                                                                 10
     179 ttatttattt
     182 <210> SEQ ID NO: 11
     183 <211> LENGTH: 18
     184 <212> TYPE: DNA
     185 <213> ORGANISM: artificial sequence
     187 <220> FEATURE:
     188 <223> OTHER INFORMATION: Forward GUS-LcF primer
     190 <400> SEQUENCE: 11
                                                                                 18
     191 atcaqcqttq gtgggaaa
     194 <210> SEQ ID NO: 12
     195 <211> LENGTH: 18
     196 <212> TYPE: DNA
     197 <213> ORGANISM: artificial sequence
     199 <220> FEATURE:
     200 <223> OTHER INFORMATION: reverse GUS-LcR primer
     202 <400> SEOUENCE: 12
                                                                                 18
     203 acgaatatct gcatcggc
     206 <210> SEQ ID NO: 13
     207 <211> LENGTH: 716
     208 <212> TYPE: DNA
     209 <213> ORGANISM: artificial sequence
     211 <220> FEATURE:
     212 <223> OTHER INFORMATION: Vigna mungo (SH-EP promoter), Bacillis amyloliquefaciens
(barnase
               gene), Esherichia coli (uidA gene)
     213
     215 <400> SEQUENCE: 13
     216 tattgaatcc tttggctacc attcttgaga aacacaaaca cttcttatat ctgttctaca
                                                                                 60
     218 caattetetg agtgegtgee acagtttggt atetteatga ttgeteattg tteatgeeca
                                                                                120
     220 taaggaacat gtaacttcct catttattta ttattgcttt tgttttcttc tcactagttt
                                                                                180
     222 acaaacgttt ccctatataa accctccttt gttcactgct ttcctccctg ctgtggcttc
                                                                                 240
     224 tetecgaagt teateceggt ecacetgeaa aataagtaat aagataaagt aaaaaagtta
                                                                                 300
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/644,664

DATE: 09/03/2003 TIME: 16:54:47

Input Set : A:\kuvshinov 1-intron.ST25.txt
Output Set: N:\CRF4\09032003\J644664.raw

226	gtatggctca	agttattaat	acttttgatg	gagttgctga	ttatcttcaa	acttatcata	360
228	aacttccaga	taattatatt	actaaatctg	aagctcaagc	tcttggatgg	gttgcttcta	420
230	aaggaaatct	tactaatatt	gctccaggaa	aatctattgg	aggagatatt	ttttcaaata	480
232	gagaaggaaa	acttccagga	aaatctggaa	gaacatggag	agaagctgat	attaattata	540
234	cttctggatt	tagaaattca	gatagaattc	tttattcatc	tgattggctt	atttataaaa	600
236	ctacagatca	ttatcaaact	tttacaaaaa	ttagataaat	atttgtattt	tttgtatgtt	660
238	gtgatcatta	ataaataaat	aaatacatac	ctcttctgca	gcaggaaggc	agccga	716

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/644,664

DATE: 09/03/2003 TIME: 16:54:48

Input Set : A:\kuvshinov 1-intron.ST25.txt
Output Set: N:\CRF4\09032003\J644664.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date